

Brain Tumor Segmentation Using Deep Learning

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Abstract

Brain tumor segmentation has been one of the most critical topics ever due to the danger it imposes on an individual's life. As with any other disease, the earlier it is diagnosed, the better the prophylactic measures that can be taken. Applying such a model would allow for a quick glance at the magnetic resonance imaging (MRI) to produce a decision. This would, in turn, reduce time within the decision-making process, allowing for more accurate and precise decisions helping doctors save more patients' lives. This paper discusses various deep learning techniques by which tumor segmentation could occur, including convolutional neural networks (CNN), enhanced convolutional neural networks (ECNN), and EnsembleNet.

Keywords: Segmentation, Brain Tumor, MRI, CNN, ECNN, EnsembleNet, Deep Learning.

Introduction

"A brain tumor is an abnormal growth or mass of cells in or around your brain". (Cleveland Clinic, 2022) Tumors are divided into malignant (cancerous) and benign (non-cancerous), where about one-third of the brain tumors are malignant. However, in both cases, it affects the functions of the brain and one's health if it grows large, pressing on surrounding nerves, blood vessels, and tissues. (Cleveland Clinic, 2022) This, in turn, gives rise to the importance of identifying a brain tumor early on to avoid its complications. Deep learning techniques have been introduced to produce quicker segmentation, providing more accurate and robust outputs. This paper aims to survey the different techniques present to solve the segmentation problem, develop the best model to carry the problem

further and update the model to achieve better results. The motivation behind this is to reduce the time taken to produce an accurate diagnosis free from human error. Hence, this model takes the MRI images as an input (*Figure 1*) and outputs the MRI with the colored tumor region (*Figure 2*). (Cleveland Clinic, 2022)

Results From The Literature

MODELS

After examining the previously published literature, it is clear that several efficient CNN architectures could be used in brain tumor segmentation.

Ben naceur et al. compared two CNN models, 2CNet and 3CNet, then proposed an ensemble of the two named EnsembleNet. (2018) This model works by taking the outputs of 2CNet and 3CNet and concatenating them together. (Ben naceur et al. 2018) *Figure 3* illustrates the architecture of this model. (Ben naceur et al. 2018) Furthermore, they suggested implementing Incremental XCNet, which simultaneously creates and trains a CNNs model with a new training approach called ELOBA $_{\lambda}$. (Ben naceur et al. 2018) The aim of using ELOBA $_{\lambda}$ was to unify the training steps for all models. (Ben naceur et al. 2018) Additionally, a non-parametric fusion function was used because it "elects only the tumor region with a high probability". (Ben naceur et al. 2018) The input to their model was a patch matrix of 32x32 pixels in four channels. (Ben naceur et al. 2018) The results were a Dice score of 0.89, 0.74 specificity, 0.82 sensitivity, 14.62 Hausdorff distance, and an inference time of 21.49 seconds to segment the whole brain.

Havaei et al. proposed using two models, TwoPathCNN and InputCascadeCNN, such that the

output of the first is used as the input for the latter. (2016) The architecture of this model can be seen in *Figure 4*. (Havaei et al., 2016; Havaei et al., 2017). It is also worth mentioning that they used stochastic gradient descent to optimize their model, which they expected would perform “poorly” due to the classes being “strongly” imbalanced. (Havaei et al., 2016) They implemented two training phases; in the first one, they constructed their training dataset with equiprobable labels, and in the second, they took into consideration the data’s unbalanced nature and re-train the output layer. (Havaei et al., 2016; Havaei et al., 2017) As a post-processing step, they pruned the highest and lowest 1% intensities and used N4ITK bias correction. (Havaei et al., 2016) For the BRATS-2013 dataset, the results were 0.88 Dice score, 0.89 specificity, and 0.87 sensitivity for the complete brain. (Havaei et al., 2016; Havaei et al., 2017) As for the BRATS-2015 dataset, the results were strongly competitive and had fewer outliers (*Figure 5*). (Havaei et al., 2016) For the SISS dataset, the average was 8.92 ASSD, 0.69 Dice score, Hausdorff distance 31.75, precision 0.72, and recall 0.67. (Havaei et al., 2016) Lastly, for the SPES dataset, the average was 1.76 ASSD, 0.85 Dice score, Hausdorff distance 23.28, precision 0.83, and recall 0.88. (Havaei et al., 2016) This model segmented the complete brain 45 times faster than if they were to implement “independent per pixel prediction”. (Havaei et al., 2016)

According to Chen et al., brain tumor segmentation aims to divide a brain tumor into four main parts (necrosis, edema, non-enhancing tumor, and enhancing tumor). These parts are observed to characterize having “Gliomas”, a common type of brain tumor. While most solutions focus on improving the quality of the features produced by the DCNN, this paper aims to find the gap in the literature where it views the problem from a different perspective using the BraTS 2015 dataset. According to Chen et al., a biological feature is shared between all the images fed into the BraTS models: that most of the tumor regions in images are left-right asymmetry. This fact pushed the researchers to explore the possibility of combining the concept of symmetry with tumor segmentation using a Deep Convolutional Neural Network, hence coming up with the Deep Convolutional Symmetric Neural Network (DCSNN).

The idea is that the input images and their left-right flip images enter the model at the same time. Then, features are extracted and used to calculate the asymmetrical location information of the input images through a similarity metric, as shown in *Figure 7*. This method determines the similarity in the created feature space and utilizes the similarity to obtain additional location data.

The data is normalized during training and testing to be between 0 and 1. This approach is based on the Baseline Network to create a more enhanced network using Left-Right Similarity Mask (LRSM), as shown in *Figure 6*. The loss function used in this paper is the commonly used softmax cross-entropy (Chen et al., 2020). The LRSM is used to add symmetry to the shared segmentation network because it gives vital location information and assigns different weights to features reflecting the symmetric location information of the input images. The results are evaluated by dice similarity coefficient metric (DSC). Since the LRSM is considered the location weight of the features, this addition significantly improved the performance of the DCNN.

This method takes almost 9.7 s to segment a patient’s brain with 155 slices. It also achieved a competitive result with an average DSC of 0.852, as shown in *Figure 8*, which compares results between the baseline model (DCNN) and the new model (DCSNN). The Deep Convolutional Symmetric Neural Network had a competitive advantage over other models that used BraTS 2015 as it only takes less than 10s to segment a patient’s brain; however, it is essential to note that this model assumes that most of the tumor regions in images are left-right asymmetry (Chen et al., 2020).

Another interesting research study by Isensee et al. used a convolutional neural network (CNN) inspired by U-Net for brain tumor segmentation and survival prediction using the BraTS 2017 dataset. Based on the U-Net model, this paper focuses on creating a robust segmentation algorithm to segment the BraTS 2017 dataset successfully. The model effectively prevents overfitting by utilizing a dice loss function to address class imbalances and heavily using data augmentation (Isensee et al., 2017).

The augmentation techniques used during training were random rotations, random scaling,

random elastic deformations, gamma correction augmentation, and mirroring. As shown in *Figure 9*, the researchers used the U-Net as our architecture's source. High-level information is gathered by the context pathway (left), while the localization pathway (right) explicitly localizes it. Deep supervision is used to introduce gradient signals deeply into the network. Additionally, the authors use radiomic features and machine learning algorithms like Random Forest and multilayer perceptrons to predict patient survival based on tumor characteristics and age, as shown in.

This method ranked number 2 worldwide on the BraTS 2015 dataset and was one of the leading methods on the BraTS 2017 challenge. Its segmentation Scores had dice scores on the validation set of 0.896 for the whole tumor, 0.797 for the tumor core, and 0.732 for the enhancing tumor (Isensee et al., 2017). As for the dice scores on the test set, it had a score of 0.858 for the whole tumor, 0.775 for the tumor core, and 0.647 for the enhancing tumor.

For its survival prediction scores, it had an accuracy of 52.6%. The approach is feasible, showing strong segmentation performance and promising results in survival prediction. It has segmentation accuracy with minimal overfitting. It also utilizes an efficient U-Net architecture for such complex medical data, integrating radiomic features for survival prediction. However, it had a lower performance in enhancing tumor segmentation, with a possibility for improvement in feature selection (Isensee et al., 2017).

Rao et al. (2015) proposed using a CNN Model that is then fed into a Random Forest to be trained. Their idea was to use a pixel-wise classification where each CNN is trained separately to identify a pixel as one of the five classes: non-tumor, necrosis, edema, non-enhancing, and enhancing. Since the BRaTS '15 was the data set used to build the model, Rao et al. (2015) made use of the multimodality information, which are the T1, T1c, T2, and Flair images, to then input each to a different CNN. As for the intermediate layers, they apply "convolution, pooling, normalization, and other operations to capture the highly nonlinear mappings between inputs and outputs" (Rao et al., 2015). ReLU was used as the activation function within the final hidden layer to improve the gradients, and then finally, the softmax was used to classify the pixel as one of the five classes. Finally, they trained the CNNs

using stochastic gradient descent where the last hidden layer represents the pixel in that modality *Figure 10*. These representations are then concatenated as features and are used to train the random forest model *Figure 11*. To test the model, they used two settings: the first was training 25,000 randomly chosen pixels, and the accuracy was 67% on the testing set. Whereas the second setting, they "trained the network using all the patches of 10 patients and were able to reach a loss of 2.9 % on the training set" (Rao et al., 2015). One notable advantage of such a model is that it can learn good representations for every pixel based on the patches extracted surrounding that pixel. As for its feasibility, it requires a workstation with 16GB of RAM and a CUDA compatible Nvidia GPU.

Another research study concerned with brain tumor segmentation was the one by Thaha et al. (2019), which proposed using an Enhanced Convolutional Neural Network model (ECNN). To start off, they had to undergo some data preprocessing regarding the images to make them suitable for further examination. This process included Skull-Stripping, which is defined as the process of "eradicating the tissues that are not cerebral" to make the cortex of the brain more visible, which can then be viewed as a unique dark ring surrounding the brain. To build up the model, they ensured that "twice the number of neurons in the output layer is set as a default number of nodes at the hidden layer" (Thaha et al., 2019). A fully connected multi-layer perceptron (MLP) was used to express the brain tumor test samples' pattern and avoid overfitting *Figure 12*. The output of the ECNN is an estimated probability of whether or not the pixel belongs to a tumor. The model utilizes a pixel-wise segmentation with a cross-entropy loss function. Since "the results from the segmentation process of CNN might not match the brain tumor category if the feather map contains the pixels that belong to other brain parts which are non-brain categories," Thaha et al. (2019) constructed a new layer for the CNN where the layer filters out the pixels that are not tumors to prevent affecting the decision, yet the layer must have the capacity to preserve the characters and textures within the map. In addition, the calculations used on the matrix now integrated the presence of the new layer *Figure 13*. To reduce the error, they even proposed using a Novel Bat Optimization Algorithm

(NBOA) where the difference between the optimal and non-optimal error is decided depending on the Echolocation mechanism, allowing it to identify the tumors more effectively. The model resulted in around 92% accuracy, 87% precision, and 90% recall. When comparing these results to the standard CNN model, ECNN has performed significantly better. While ECNN performs exceptionally well in the evaluation metrics, its dependency on the quality and quantity of the training data could be somewhat of a huge disadvantage since we cannot always control the quality of data.

DATASETS

Several datasets were used, such as the BRATS-2013, BRATS-2015, BRATS-2017, sub-acute ischemic stroke lesion segmentation (SISS), and acute stroke outcome/penumbra estimation (SPES) datasets. It is essential to note that some of these datasets are inaccessible due to being part of competitions conducted previously; therefore, the datasets' descriptions will be extracted from previous publications instead.

The BRATS-2013 dataset consists of 40 brain images divided into training and testing sets. (Havaei et al., 2016) The training set contains 20 high-grade gliomas and ten low-grade gliomas, while the testing set contains ten high-grade gliomas. (Havaei et al., 2016)

Furthermore, the BRATS-2015 dataset is also divided into training and testing sets, which contain 274 and 53 images, respectively. (Havaei et al., 2016) The training set includes 54 low-grade brains and 220 high-grade brains. (Havaei et al., 2016) It is also worth mentioning that the BRATS-2015 dataset contains the training set from BRATS-2013. (Havaei et al., 2016)

The BRATS-2017 dataset has MRIs for 285 patients, 210 of whom have high-grade Glioblastomas, and the remaining 75 have low-grade Glioblastomas. (Ben naceur et al. 2018)

It is worth noting that, for all the BRATS datasets, each image comes in four "modalities": "T1, T1[C], T2, [F]lair". (Ben naceur et al. 2018) (Havaei et al., 2016) In addition, they have "[five] segmentation labels, namely healthy, necrosis, edema, non-enhancing tumor and enhancing tumor". (Havaei et al., 2016)

The SISS dataset consists of 28 brain images. (Havaei et al., 2016) The images are categorized as "Flair, Diffusion Weighted Image (DWI) and T1," which can be seen in *Figure 14* alongside the ground truth. (Havaei et al., 2016)

Lastly, when it comes to the SPES dataset contains 30 MRI images where each brain has seven modalities, which are the following: "CBF (Cerebral blood flow), CBV (cerebral blood volume), DWI (diffusion-weighted images), T1c, T2, Tmax and TTP (time to peak)". (Havaei et al., 2016) An example of this dataset is illustrated in *Figure 15*. (Havaei et al., 2016)

Chosen Dataset

We plan on using the BRATS-2020 dataset. The Brain Tumor Segmentation (BraTS) 2020 dataset is a collection of multimodal Magnetic Resonance Imaging (MRI) scans used for segmenting brain tumors. The full dataset is inaccessible due to being part of competitions conducted previously; however, we were able to obtain a version that has most of the data, with a few missing data entries that we can deal with.

This dataset consists of 369 Brain MRI Images. The dataset file contains 57195 images and four primary files: BraTS20 Training Metadata, survival_info, name_mapping, and meta_data. The images map out to MRI scans of slices of the brain of 369 patients, saved as .h5 files. Every 155 image slice reflects one patient; therefore, 155 slices * 369 patients give 57195 images.

Our dataset consists of images from brain scans, as well as masked labels indicating regions of abnormal tissue. Each image has four channels.

1. T1-weighted (T1): This sequence produces a high-resolution image of the brain's anatomy. It is suitable for visualizing the brain's structure but less sensitive to tumor tissue than other sequences.
2. T1-weighted post-contrast (T1c or T1Gd) is useful for highlighting malignant tumors.
3. T2-weighted (T2): T2 images provide excellent contrast of the brain's fluid spaces and are sensitive to edema (swelling), which often surrounds tumors.
4. Fluid Attenuated Inversion Recovery (FLAIR): This sequence suppresses the fluid signal, making it easier to see peritumoral edema (swelling around the tumor).

The masks represent segmentations, containing areas of interest within the brain scans. They specifically focus on abnormal tissue related to brain tumors. These masks can be used to train models in segmenting brain tumors from normal brain tissue. Each mask has three channels.

1. Necrotic and Non-Enhancing Tumor Core (NCR/NET): This masks out the necrotic (dead) part of the tumor, which includes healthy brain tissue or non-tumor regions.
2. Edema (ED): This channel masks the edema, swelling, or fluid accumulation around the tumor.
3. Enhancing Tumor (ET): This masks out the enhancing tumor, which is the tumor region that shows uptake of contrast material and is often considered the most aggressive part of the tumor.

The BraTS20 Training Metadata file contains 57195 data points and eight variables:

- Slice_path
- Target
- Volume
- Slice
- Label0_pxl_cnt
- Label1_pxl_cnt
- Label2_pxl_cnt
- Background_ratio

The slice_path reflects the name and file path of the image inside the dataset. The target shows 0 or 1 depending on whether or not the brain is tumorous. 158 patients are labeled with tumors, while 211 are labeled non-tumorous.

The volume refers to the 3D MRI volume (or the patient scan) from which the 2D slice was extracted. Each volume contains multiple 2D slices, and the volume provides context for which patient or scan the slice belongs to. The slice indicates the slice number within the 3D volume. For instance, if a volume contains 100 slices, this could be slice number 45 out of 100, indicating its position in the series. Label0_pxl_cnt is a number of pixels in the slice that correspond to areas of interest of abnormal tissue, and the same for the rest of the labels.

- Label0_pxl: Not Tumor (NT) volume
- Label1_pxl: Edema (ED)
- Label2_pxl: Enhancing Tumor (ET)

The background ratio is the ratio of pixels in the slice that belong to the background or areas that are not part of the tumor (such as normal brain tissue or other non-tumor regions).

The name_mapping consists of the Grade of the image, which is categorized as High-Grade Gliomas (HGG) or Low-Grade Gliomas (LGG), which exhibit different growth patterns and clinical impacts. This dataset has 77 LGG patients and 283 HGG patients. It also contains the image ID in the BraTS 2018, 2019, and 2020 in case the same image was used in previous datasets.

The survival info file contains the Age, Survival days, and Extent of resection (an indicator of whether or not the patient will survive longer).

Lastly, the meta_data contains the slice path, target, volume, and slice, which are all redundant with the BraTS20 Training Metadata.

This dataset is ideal because it contains a large and diverse set of patients with varying tumor grades (HGG and LGG), which ensures that models trained on it can generalize better across different clinical settings. In addition, it is labeled and contains lots of data about the brain scans, which can help us map out the segmentation. Lastly, the dataset needs to have the problem of class imbalance, which will help us achieve a smooth modeling process.

Therefore, this dataset can support the development of high-accuracy models capable of assisting in diagnosis, treatment planning, and disease monitoring, making it invaluable for medical imaging research and real-world applications.

Chosen Model

After thoroughly analyzing the aforementioned evidence, we chose the TwoPathsCNN model, which is joined at various positions, as our baseline model. This type of model has a cascading architecture, which means that two inputs are to be taken from the image and then assembled after several activation functions to have the output of one model be the input of the next one, as described in *Figure 16*.

Proposed Updates

PROPOSED BASELINE MODEL UPDATES

We propose adjusting this model so it fits our dataset (BRATS-2020) instead of the

BRATS-2013. We will incorporate attention gates into the model architecture to be able to focus on the most relevant regions of the MRI images. We will use U-Net as the base model due to its effectiveness in medical image segmentation, as it is particularly suited for capturing the intricate details of MRI images. In addition, we plan on using the Two-Path CNN model. To complement the strength of the Two-Path CNN, we plan to feed it into the U-Net model, where the extracted features from Two-Path CNN can be used as the input of the downsampling path. The next step would be merging the feature maps from the downsampling path using the skip connections of U-Net. This would allow for a reduction of the spatial dimensions while increasing the feature depth, allowing for precise tumor segmentation. As an extra mile, we could try to incorporate a model where all modalities are to be fed into one model only instead of building a model for each modality and concatenating them at the end.

Additionally, we will adapt the code output to be binary, focusing on the presence or absence of a tumor rather than predicting one of the five classes in the baseline model. In addition, we intend to note the stochastic gradient descent application's drawbacks and limitations, which include its poor performance in the case of class imbalance. This class imbalance is inevitable because even in the images that contain a brain tumor, the majority of the pixels in this image are healthy. Therefore, we propose using mini-batch gradient descent to adjust the weights of our model. Another proposed update that could be done during the pre-processing part is the Skull-Stripping technique, which we could use to enhance the images' quality, thus increasing the performance of our model.

PROPOSED EVALUATION METRICS

Furthermore, to evaluate this proposition, we suggest using the Dice score, specificity, and sensitivity as the evaluation methods. We consider that these are the metrics often used when examining various resources, so using the same ones would allow us to compare our results with the literature. In addition, we will construct a confusion matrix to assess how well the model can classify each class correctly.

Graduation Project

Our proposed graduation project topic lies under the Natural Language Processing (NLP) topic,

where we aim to identify words written in Franco/Arabizi, defined as using Latin letters to write Arabic words. This word disambiguation process would mainly aid in doing market research on products by mining people's feedback, written in Franco/Arabizi, from any social media platform to conduct sentiment analysis on this feedback. Next, a real-time report is generated, including dashboards about the feedback received, what could be improved, and customer segmentation. This would, in turn, help the marketing team evaluate their company's products and even assess how they are doing with respect to their competitors.

Conclusion

After careful consideration of all aforementioned points, it is irrefutable that brain tumor segmentation is a crucial task in medical imaging, with significant implications for early diagnosis and treatment planning. Deep learning models, particularly convolutional neural networks (CNNs), have shown great potential in automating this process by providing fast, accurate, and robust segmentation results. The literature demonstrates the success of various CNN architectures, including EnsembleNet, TwoPathCNN, and Deep Convolutional Symmetric Neural Networks, each offering unique approaches to enhance segmentation accuracy, reduce inference time, and address challenges like class imbalance.

The BraTS datasets have been instrumental in advancing the field, offering multimodal MRI data that reflect real-world clinical scenarios. Many updated model innovations improved Dice scores and accuracy across different tumor regions.

While significant progress has been made, challenges remain in achieving optimal segmentation for brain tumors. We propose to work on TwoPathCNN and U-Net baseline models to be able to achieve a more robust model to be able to generalize the model across another dataset (BraTS, 2020) and improve its metrics. We will add attention gates and use stochastic gradient descent to improve the model. By addressing these challenges, our research on deep learning models can continue to enhance brain tumor segmentation, ultimately improving patient outcomes and enabling faster, more accurate medical decisions.

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Appendices

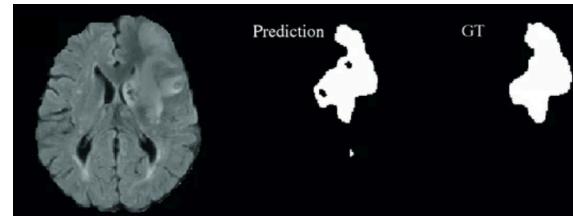


Figure 1: The input images to the model

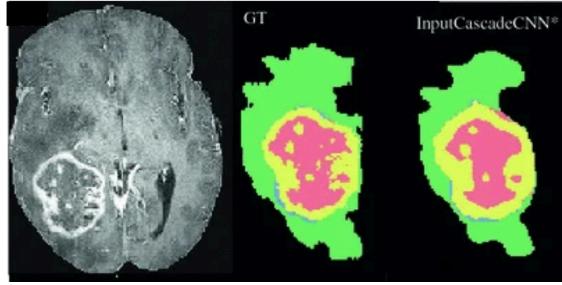


Figure 2: The output of the model

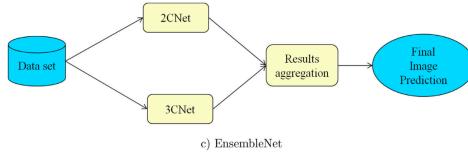


Figure 3: Simple architecture of EnsembleNet

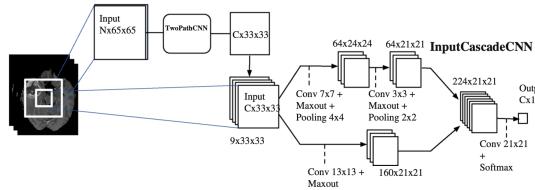


Figure 4: Architecture of model containing TwoPathCNN and InputCascadeCNN

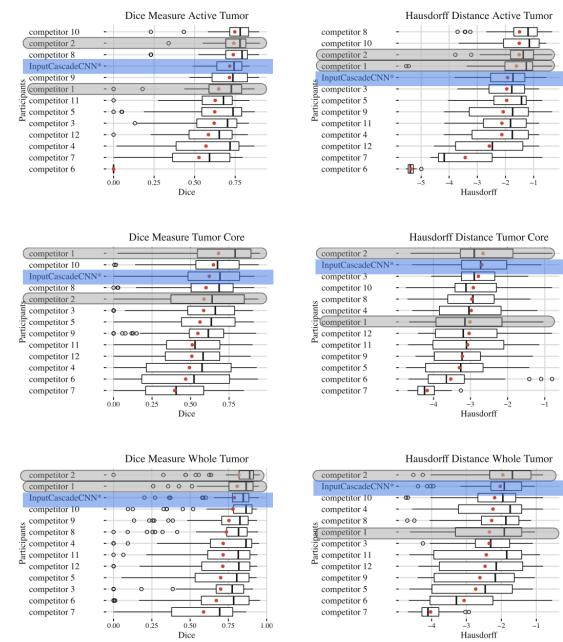
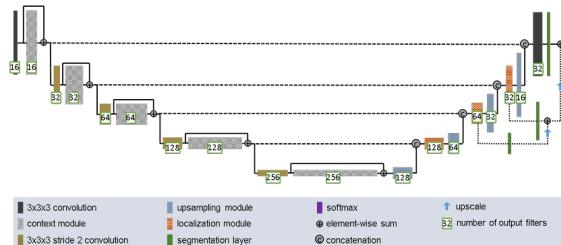


Figure 5: BRATS-2015 results of InputCascadeCNN

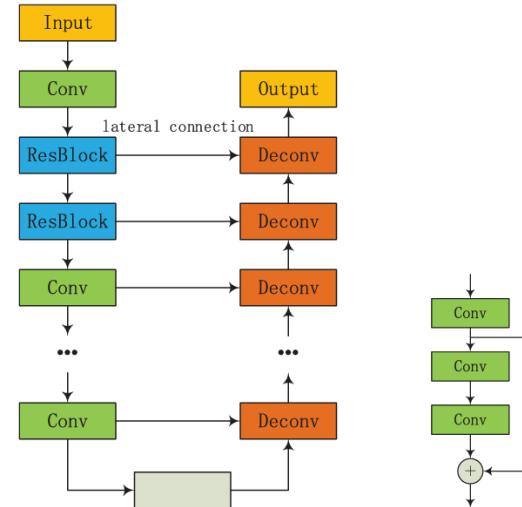


Figure 6: (a) Architecture of the Baseline Network
(b) Architecture of ResBlock

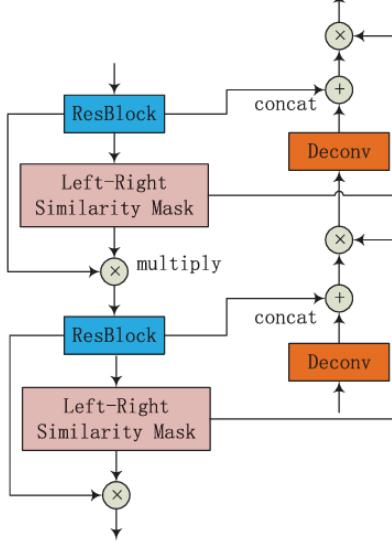


Figure 7: Architecture of Deep Convolutional Symmetric Neural Network

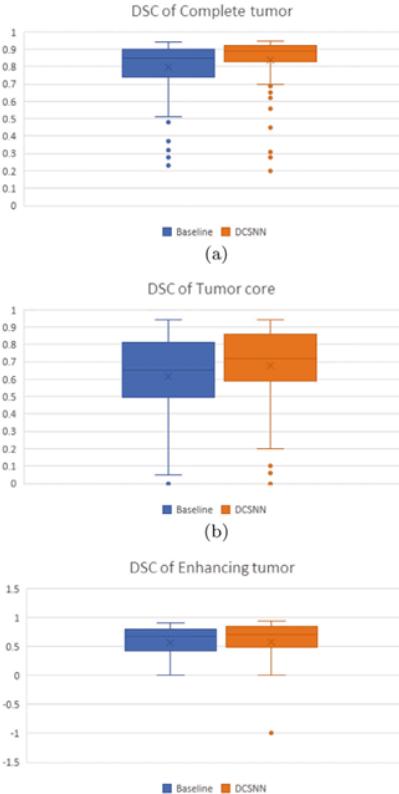


Figure 8: Comparison between Baseline model and DCSNN results

Figure 9: Architecture of model based on the U-Net

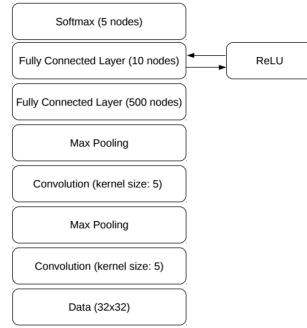


Figure 10: Architecture of each convolutional neural network to be fed into the random forest

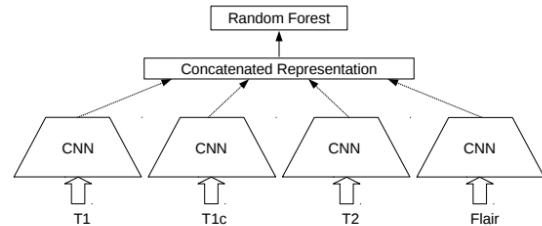


Figure 11: Architecture of the concatenation of CNN into the Random Forest model.

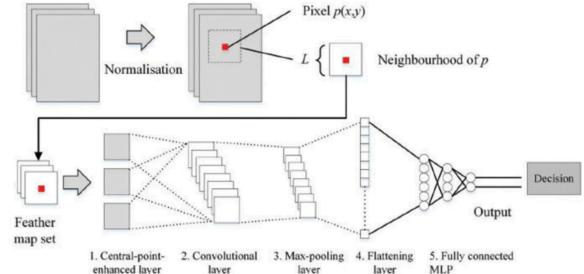


Figure 12: Architecture of Enhanced Convolutional Neural Network (ECNN) Model.

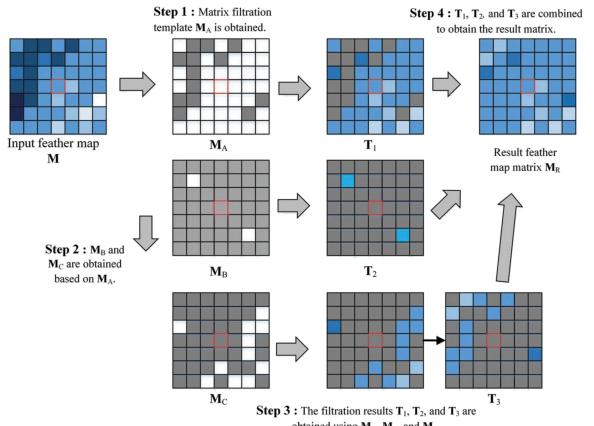


Figure 13: New layer constructed for CNN to avoid the mismatch of the brain category

- Results from the literature for two sources
- Chosen model
- Proposed updates

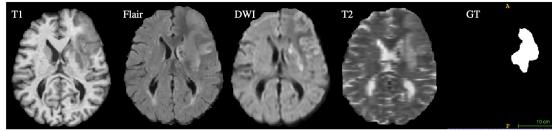


Figure 14: SISS dataset example with the four modalities and the ground truth

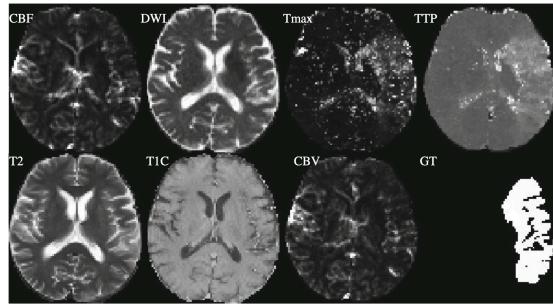


Figure 15: SPES dataset example with the seven modalities and the ground truth

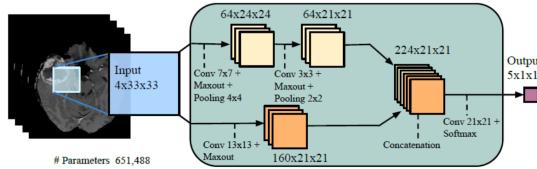


Figure 16: TwoPathsCNN model architecture

Team Contribution

Farida:

- Summarizing two sources
- Results from literature for two sources
- Datasets descriptions for BRATS-2013, BRATS-2015, BRATS-2017, SISS, and SPES
- Evaluation metrics
- References
- Proofreading
- Chosen Model
- Proposed updates

Mona:

- Summarizing two sources
- Results from the literature for two sources
- Chosen dataset
- Conclusion
- Chosen model
- Proposed updates

Sama:

- Summarizing three sources
- Abstract
- Introduction
- Graduation Project description